

CW

Serial Number: 01/831426

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: PH#16
- ☐ Edited the Current Application Data section with the actual current number. The number input applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings added included: **ENTERED**
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename or ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first C
Action. DO NOT send a copy of this form.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,426

DATE: 11/19/2001

TIME: 14:12:38

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Output Set: N:\CRF3\11192001\I831426.raw

NOV 20 2002

TECH CENTER 1600/2900

4 <110> APPLICANT: Hoechst Marion Roussel
 5 Bordon-Pallier, F.
 6 Rocher, C.
 8 <120> TITLE OF INVENTION: Human htFIIIA gene and coded htFIIIA protein
 10 <130> FILE REFERENCE: 146.1364
 12 <140> CURRENT APPLICATION NUMBER: US 09/831,426
 13 <141> CURRENT FILING DATE: 2001-05-08
 15 <160> NUMBER OF SEQ ID NOS: 10
 17 <170> SOFTWARE: PatentIn Vers. 2.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1273
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Human
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (176)..(1270)
 28 <400> SEQUENCE: 1

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 33 acgtgtctcg gcacgtggca gcgcgcctgg ccctgggctt ggaggcgccg gcgcc ctg 178
 34 Met
 35 1
 37 gat ccg ccg gcc gtg gtc gcc gag tcg gtg tcg tcc ttg acc atc gcc 226
 38 Asp Pro Pro Ala Val Val Ala Glu Ser Val Ser Ser Leu Thr Ile Ala
 39 5 10 15
 41 gac gcg ttc att gca gcc ggc gag agc tca gct ccg acc ccg ccg cgc 274
 42 Asp Ala Phe Ile Ala Ala Gly Glu Ser Ser Ala Pro Thr Pro Pro Arg
 43 20 25 30
 45 ccc gcg ctt ccc agg agg ttc atc tgc tcc ttc cct gac tgc agc gcc 322
 46 Pro Ala Leu Pro Arg Arg Phe Ile Cys Ser Phe Pro Asp Cys Ser Ala
 47 35 40 45
 49 aat tac agc aaa gcc tgg aag ctt gac gcg cac ctg tgc aag cac acg 370
 50 Asn Tyr Ser Lys Ala Trp Lys Leu Asp Ala His Leu Cys Lys His Thr
 51 50 55 60 65
 53 ggg gag aga cca ttt gtt tgt gac tat gaa ggg tgt ggc aag gcc ttc 418
 54 Gly Glu Arg Pro Phe Val Cys Asp Tyr Glu Gly Cys Gly Lys Ala Phe
 55 70 75 80
 57 atc agg gac tac cat ctg agc cgc cac att ctg act cac aca gga gaa 466
 58 Ile Arg Asp Tyr His Leu Ser Arg His Ile Leu Thr His Thr Gly Glu
 59 85 90 95
 61 aag ccg ttt gtt tgt gca gcc act ggc tgt gat caa aaa ttc aac aca 514
 62 Lys Pro Phe Val Cys Ala Ala Thr Gly Cys Asp Gln Lys Phe Asn Thr
 63 100 105 110
 65 aaa tca aac ttg aag aaa cat ttt gaa cgc aaa cat gaa aat caa caa 562
 66 Lys Ser Asn Leu Lys Lys His Phe Glu Arg Lys His Glu Asn Gln Gln
 67 115 120 125
 69 aaa caa tat ata tgc agt ttt gaa gac tgt aag aag acc ttt aag aaa 610

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70 Lys Gln Tyr Ile Cys Ser Phe Glu Asp Cys Lys Lys Thr Phe Lys Lys
71 130                      135                      140                      145
73 cat cag cag ctg aaa atc cat cag tgc cag cat acc aat gaa cct cta 658
74 His Gln Gln Leu Lys Ile His Gln Cys Gln His Thr Asn Glu Pro Leu
75                      150                      155                      160
77 ttc aag tgt acc cag gaa gga tgt ggg aaa cac ttt gca tca ccc agc 706
78 Phe Lys Cys Thr Gln Glu Gly Cys Gly Lys His Phe Ala Ser Pro Ser
79                      165                      170                      175
81 aag ctg aaa cga cat gcc aag gcc cac gag ggc tat gta tgt caa aaa 754
82 Lys Leu Lys Arg His Ala Lys Ala His Glu Gly Tyr Val Cys Gln Lys
83                      180                      185                      190
85 gga tgt tcc ttt gtg gca aaa aca tgg acg gaa ctt ctg aaa cat gtg 802
86 Gly Cys Ser Phe Val Ala Lys Thr Trp Thr Glu Leu Leu Lys His Val
87                      195                      200                      205
89 aga gaa acc cat aaa gag gaa ata cta tgt gaa gta tgc cgg aaa aca 850
90 Arg Glu Thr His Lys Glu Glu Ile Leu Cys Glu Val Cys Arg Lys Thr
91 210                      215                      220                      225
93 ttt aaa cgc aaa gat tac ctt aag caa cac atg aaa act cat gcc cca 898
94 Phe Lys Arg Lys Asp Tyr Leu Lys Gln His Met Lys Thr His Ala Pro
95                      230                      235                      240
97 gaa agg gat gta tgt cgc tgt cca aga gaa ggc tgt gga aga acc tat 946
98 Glu Arg Asp Val Cys Arg Cys Pro Arg Glu Gly Cys Gly Arg Thr Tyr
99                      245                      250                      255
101 act act gtg ttt aat ctc caa agc cat atc ctc tcc ttc cat gag gaa 994
102 Thr Thr Val Phe Asn Leu Gln Ser His Ile Leu Ser Phe His Glu Glu
103                      260                      265                      270
105 agc cgc cct ttt gtg tgt gaa cat gct ggc tgt ggc aaa aca ttt gca 1042
106 Ser Arg Pro Phe Val Cys Glu His Ala Gly Cys Gly Lys Thr Phe Ala
107                      275                      280                      285
109 atg aaa caa agt ctc act agg cat gct gtt gta cat gat cct gac aag 1090
110 Met Lys Gln Ser Leu Thr Arg His Ala Val Val His Asp Pro Asp Lys
111 290                      295                      300                      305
113 aag aaa atg aag ctc aaa gtc aaa aaa tct cgt gaa aaa cgg agt ttg 1138
114 Lys Lys Met Lys Leu Lys Val Lys Lys Ser Arg Glu Lys Arg Ser Leu
115                      310                      315                      320
117 gcc tct cat ctc agt gga tat atc cct ccc aaa agg aaa caa ggg caa 1186
118 Ala Ser His Leu Ser Gly Tyr Ile Pro Pro Lys Arg Lys Gln Gly Gln
119                      325                      330                      335
121 ggc tta tct ttg tgt caa aac gga gag tca ccc aac tgt gtg gaa gac 1234
122 Gly Leu Ser Leu Cys Gln Asn Gly Glu Ser Pro Asn Cys Val Glu Asp
123                      340                      345                      350
125 aag atg ctc tcg aca gtt gca gta ctt acc ctt ggc taa 1273
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131 <211> LENGTH: 365
132 <212> TYPE: PRT
133 <213> ORGANISM: Human
135 <400> SEQUENCE: 2

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137   1           5           10           15
139 Ala Asp Ala Phe Ile Ala Ala Gly Glu Ser Ser Ala Pro Thr Pro Pro
140           20           25           30
142 Arg Pro Ala Leu Pro Arg Arg Phe Ile Cys Ser Phe Pro Asp Cys Ser
143           35           40           45
145 Ala Asn Tyr Ser Lys Ala Trp Lys Leu Asp Ala His Leu Cys Lys His
146           50           55           60
148 Thr Gly Glu Arg Pro Phe Val Cys Asp Tyr Glu Gly Cys Gly Lys Ala
149   65           70           75           80
151 Phe Ile Arg Asp Tyr His Leu Ser Arg His Ile Leu Thr His Thr Gly
152           85           90           95
154 Glu Lys Pro Phe Val Cys Ala Ala Thr Gly Cys Asp Gln Lys Phe Asn
155           100          105          110
157 Thr Lys Ser Asn Leu Lys Lys His Phe Glu Arg Lys His Glu Asn Gln
158           115          120          125
160 Gln Lys Gln Tyr Ile Cys Ser Phe Glu Asp Cys Lys Lys Thr Phe Lys
161           130          135          140
163 Lys His Gln Gln Leu Lys Ile His Gln Cys Gln His Thr Asn Glu Pro
164 145           150          155          160
166 Leu Phe Lys Cys Thr Gln Glu Gly Cys Gly Lys His Phe Ala Ser Pro
167           165          170          175
169 Ser Lys Leu Lys Arg His Ala Lys Ala His Glu Gly Tyr Val Cys Gln
170           180          185          190
172 Lys Gly Cys Ser Phe Val Ala Lys Thr Trp Thr Glu Leu Leu Lys His
173           195          200          205
175 Val Arg Glu Thr His Lys Glu Glu Ile Leu Cys Glu Val Cys Arg Lys
176           210          215          220
178 Thr Phe Lys Arg Lys Asp Tyr Leu Lys Gln His Met Lys Thr His Ala
179 225           230          235          240
181 Pro Glu Arg Asp Val Cys Arg Cys Pro Arg Glu Gly Cys Gly Arg Thr
182           245          250          255
184 Tyr Thr Thr Val Phe Asn Leu Gln Ser His Ile Leu Ser Phe His Glu
185           260          265          270
187 Glu Ser Arg Pro Phe Val Cys Glu His Ala Gly Cys Gly Lys Thr Phe
188           275          280          285
190 Ala Met Lys Gln Ser Leu Thr Arg His Ala Val Val His Asp Pro Asp
191           290          295          300
193 Lys Lys Lys Met Lys Leu Lys Val Lys Lys Ser Arg Glu Lys Arg Ser
194 305           310          315          320
196 Leu Ala Ser His Leu Ser Gly Tyr Ile Pro Pro Lys Arg Lys Gln Gly
197           325          330          335
199 Gln Gly Leu Ser Leu Cys Gln Asn Gly Glu Ser Pro Asn Cys Val Glu
200           340          345          350
202 Asp Lys Met Leu Ser Thr Val Ala Val Leu Thr Leu Gly
203           355          360          365
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 1273
208 <212> TYPE: DNA

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209 <213> ORGANISM: Human

211 <400> SEQUENCE: 3

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216 acgtgtctcg gcacgtggca gcgcgcctgg ccctgggctt ggaggcgccg gcgccctgga 180
218 tccgcgcggc gtggtgcgcg agtcggtgtc gtccttgacc atgcgcgacg cgttcattgc 240
220 agccggcgag agctcagctc cgaccccgcc gcgccccgcg ctcccagga gggtcatctg 300
222 ctccctccct gactgcagcg ccaattacag caaagcctgg aagcttgacg cgcacctgtg 360
224 caagcacacg ggggagagac catttgtttg tgactatgaa ggggtgtggc aggccttcat 420
226 cagggactac catctgagcc gccacattct gactcacaca ggagaaaagc cgtttgtttg 480
228 tgcagccact ggctgtgatc aaaaattcaa cacaaaatca aacttgaaga aacattttga 540
230 acgcaaacat gaaaatcaac aaaaacaata tatatgcagt tttgaagact gtaagaagac 600
232 ctttaagaaa catcagcagc tgaaaatcca tcagtgcag cataccaatg aacctctatt 660
234 caagtgtacc caggaaggat gtgggaaaca ctttgcata cccagcaagc tgaaacgaca 720
236 tgccaaggcc cagcagggct atgtatgtca aaaaggatgt tcctttgttg caaaaacatg 780
238 gacggaactt ctgaaacatg tgagagaaac ccataaagag gaaatactat gtgaagtatg 840
240 ccggaanaaa tttaaacgca aagattacct taagcaacac atgaaaactc atgccccaga 900
242 aagggatgta tgtcgtgtgc caagagaagg ctgtggaaga acctatacta ctgtgtttaa 960
244 tctccaaagc catatcctct ccttccatga ggaaagccgc ccttttgtgt gtgaacatgc 1020
246 tggctgtggc aaaacatttg caatgaaaca aagtctcact aggcattgctg ttgtacatga 1080
248 tcctgacaag aagaaaatga agctcaaagt caaaaaatct cgtgaaaaac ggagtttggc 1140
250 ctctcatctc agtgatata tccctcccaa aaggaaacaa gggcaaggct tatctttgtg 1200
252 tcaaaacgga gagtcacca actgtgtgga agacaagatg ctctcgacag ttgcagtact 1260
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1273

257 <210> SEQ ID NO: 4

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259 <212> TYPE: DNA

260 <213> ORGANISM: Human

262 <400> SEQUENCE: 4

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267 tccgcgcggc gtggtgcgcg agtcggtgtc gtccttgacc atgcgcgacg cgttcattgc 180
269 agccggcgag agctcagctc cgaccccgcc gcgccccgcg ctcccagga gggtcatctg 240
271 ctccctccct gactgcagcg ccaattacag caaagcctgg aagcttgacg cgcacctgtg 300
273 caagcacacg ggggagagac catttgtttg tgactatgaa ggggtgtggc aggccttcat 360
275 cagggactac catctgagcc gccacattct gactcacaca ggagaaaagc cgtttgtttg 420
277 tgcagccact ggctgtgatc aaaaattcaa cacaaaatca aacttgaaga aacattttga 480
279 acgcaaacat gaaaatcaac aaaaacaata tatatgcagt tttgaagact gtaagaagac 540
281 ctttaagaaa catcagcagc tgaaaatcca tcagtgcag cataccaatg aacctctatt 600
283 caagtgtacc caggaaggat gtgggaaaca ctttgcata cccagcaagc tgaaacgaca 660
285 tgccaaggcc cagcagggct atgtatgtca aaaaggatgt tcctttgttg caaaaacatg 720
287 gacggaactt ctgaaacatg tgagagaaac ccataaagag gaaatactat gtgaagtatg 780
289 ccggaanaaa tttaaacgca aagattacct taagcaacac atgaaaactc atgccccaga 840
291 aagggatgta tgtcgtgtgc caagagaagg ctgtggaaga acctatacta ctgtgtttaa 900
293 tctccaaagc catatcctct ccttccatga ggaaagccgc ccttttgtgt gtgaacatgc 960
295 tggctgtggc aaaacatttg caatgaaaca aagtctcact aggcattgctg ttgtacatga 1020
297 tcctgacaag aagaaaatga agctcaaagt caaaaaatct cgtgaaaaac ggagtttggc 1080
299 ctctcatctc agtgatata tccctcccaa aaggaaacaa gggcaaggct tatctttgtg 1140
301 tcaaaacgga gagtcacca actgtgtgga agacaagatg ctctcgacag ttgcagtact 1200

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317 <212> TYPE: DNA	
318 <213> ORGANISM: Human	
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325 <211> LENGTH: 20	
326 <212> TYPE: DNA	
327 <213> ORGANISM: Human	
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352 <211> LENGTH: 30	
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354 <213> ORGANISM: Human	
356 <400> SEQUENCE: 10	
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/831,426

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